

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 14, 2003, 00:49:36 ; search time 166.888 seconds  
(without alignments)  
1569.471 Million cell updates/sec

Title: US-09-698-781-17

Perfect score: 44

Sequence: 1 TLFPVLFL 9

Scoring table: BLOSUM62  
Xgapext 10.0 , Xgapext 0.5  
Ygapext 10.0 , Ygapext 0.5  
Fgapext 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=t -CDI -LIST=45
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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6: gb\_sts: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: qb\_pr: \*  
10: qb\_ro: \*  
11: qb\_sts: \*  
12: qb\_sy: \*  
13: qb\_un: \*  
14: qb\_vl: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_on: \*  
21: em\_or: \*  
22: em\_cv: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	44	100.0	2128	HSSPG8 H_sapiens m
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4	44	100.0	2144	AX127587 Sequence AX127587 Human DNA
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6	44	100.0	107625	AC103066 Rattus no
7	44	100.0	116742	AC069197 Homo sapi
8	44	100.0	136129	AC011050 Homo sapi
9	44	100.0	151752	AC010779 Homo sapi
10	44	100.0	152908	AC025842 Homo sapi
11	44	100.0	153003	AC094798 Rattus no
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14	44	100.0	249084	AC121977 Mus muscu
15	43	97.7	585585	AC024105 Homo sapi
16	43	97.7	165158	AC101384 Rattus no
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19	42	95.5	111701	AC130506 Rattus no
20	42	95.5	123947	AC005045 Homo sapi
21	42	95.5	175021	AC098138 Rattus no
22	42	95.5	175744	AC109189 Mus muscu
23	42	95.5	237727	AC099321 Rattus no
24	42	95.5	337133	AC110884 Rattus no
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29	41	93.2	2602	AK09857 Homo sapi
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31	41	93.2	2858	AL833616 Homo sapi
32	41	93.2	2952	AF039019 Homo sapi
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46	41	93.2	137247	AC015865 Homo sapi

#### ALIGNMENTS







Douthwaite, K.J., Draper, H., Duan-Rocha, S., Durbin, K.J.,	1242	2424:	contig of 1183 bp in length
Earnhardt, C., Edgar, D., Edwards, C.C., Elhai, C., Escotto, M.,	2425	2524:	gap of unknown length
Fallis, T., Ferradoto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,	2525	3589:	contig of 1064 bp in length
Gabis, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,	3589	3688:	gap of unknown length
Gorrell, J.H., Guerra, W., Gunaratne, P., Hale, S., Hamilton, K.,	3689	5276:	contig of 1588 bp in length
Harris, C., Harris, K., Hart, M., Havlik, P., Hawes, A., Hernandez, J.,	5277	5376:	gap of unknown length
Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,	5377	6534:	contig of 1158 bp in length
Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,	6535	6634:	gap of unknown length
Jacobsen, B., Jia, Y., Johnson, R., Jolivet, S., Joudan, S.,	6635	7795:	contig of 1161 bp in length
Karlsson, E., Kelly, S., Khan, U., King, L., Kovar, C.,	7796	7895:	gap of unknown length
Kratovic, J., Kuleshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,	7896	8986:	contig of 1091 bp in length
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louisegd, H.,	8987	9086:	gap of unknown length
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,	9087	10789:	contig of 1703 bp in length
Maheshwari, M., Mapua, S., Martin, R., Martindale, A., Martinez, P.,	10790	10899:	gap of unknown length
Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Metzler, M.,	10890	11971:	contig of 1082 bp in length
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,	11972	12071:	gap of unknown length
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,	12072	13077:	contig of 1006 bp in length
Nouyen, N., Nickerson, E., Nwokonwo, S., Ouh, M., Okwunuo, G.,	13078	13777:	gap of unknown length
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,	13778	14680:	contig of 1503 bp in length
Peters, L., Pickens, R., Primus, E., Puhl, L., Quiles, M., Ren, Y.,	14780:	15868:	gap of unknown length
Rives, M., Rojas, A., Rojubon, J., Rolfe, M., Ruiz, S., Savery, G.,	14781	15868:	contig of 1088 bp in length
Scherer, S., Scott, G., Shen, H., Shoshtari, N., Sisson, I.,	15869	15968:	gap of unknown length
Sodergren, E., Sonaike, T., Sparks, A., Stanley, R., Stone, H.,	15969:	17569:	contig of 1601 bp in length
Sutton, A., Svatek, A., Tabor, P., Tamerska, K., Tang, H.,	17570	17669:	gap of unknown length
Tansey, J., Taylor, C., Taylor, T., Teiford, B., Thomas, N., Thomas, S.,	17670	19184:	contig of 1515 bp in length
Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,	19184:	19285:	gap of unknown length
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,	19285	20795:	contig of 1511 bp in length
Williams, G., Williamson, A., Wlezyk, R., Woodin, S., Worley, K.,	20796	22056:	contig of 1561 bp in length
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,	22056:	22556:	gap of unknown length
Weinstock, G., and Gibbs, R.	22557	23586:	conting of 1030 bp in length
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\* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
 \* NOTE: This is a working draft sequence. It currently  
 \* consists of 68 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1141: contig of 1141 bp in length  
 \* 1142: gap of unknown length



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Length: 116742
Matches: 9
Conservative: 0
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Gaps: 0

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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
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AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP1-9P22
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 136129)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Birren,N., Beckerly,R., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
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Peterson,K., Poliak,V., Riley,R., Roy,A., Santos,R., Severy,P.,

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TITLE Direct Submission  
 JOURNAL Submitted (16-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 REFERENCE 3 (bases 1 to 152905)  
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Baran, N., Bastien, V., Boguslavsky, L., Boukigetter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearfield, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Larocque, K., Lamazares, R., Landers, T., Lebochky, J., Levine, R., Liu, G., MacLean, C., McDonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneus, L., Minova, T., Milena, V., Murphy, T., Nayior, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Polara, V., Raymond, C., Rettig, R., Rileback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rossetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stofanovic, N., Straus, N., Subramanian, J., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
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 JOURNAL Submitted (15-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 COMMENT On Feb 3, 2002 this sequence version replaced g1:18450159.  
 All repeats were identified using RepeatMasker:  
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 /complement(32443..34629)



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40281:	contig of 2422 bp in length	*	122666	12465: gap of unknown length
40182:	gap of unknown length	*	124766	127338: contig of 2573 bp in length
40282:	contig of 1387 bp in length	*	127339	127338: contig of 2573 bp in length
41668:	gap of unknown length	*	127439	127439: gap of unknown length
41669:	contig of 2885 bp in length	*	128568	128667: gap of unknown length
41768:	contig of 2970 bp in length	*	128668	128667: gap of unknown length
41769:	gap of unknown length	*	128922	128922: contig of 1255 bp in length
44738:	contig of 2456 bp in length	*	129923	129922: contig of 1255 bp in length
44838:	gap of unknown length	*	130022	gap of unknown length
44839:	contig of 3032 bp in length	*	130023	131375: contig of 1353 bp in length
47294:	contig of 2456 bp in length	*	131376	131375: gap of unknown length
47295:	gap of unknown length	*	131476	131476: contig of 1529 bp in length
47394:	contig of 2885 bp in length	*	133004	133004: gap of unknown length
50279:	gap of unknown length	*	133104	133104: gap of unknown length
50280:	contig of 3032 bp in length	*	133105	133104: contig of 1500 bp in length
53411:	gap of unknown length	*	133105	133104: contig of 1500 bp in length
53511:	contig of 3341 bp in length	*	134605	134604: gap of unknown length
53512:	gap of unknown length	*	134705	136591: contig of 1687 bp in length
55852:	contig of 2504 bp in length	*	136591	136591: gap of unknown length
56953:	gap of unknown length	*	136492	136492: contig of 1003 bp in length
59457:	contig of 2735 bp in length	*	137495	137494: gap of unknown length
59556:	gap of unknown length	*	137495	137494: gap of unknown length
62291:	contig of 3480 bp in length	*	137495	137494: gap of unknown length
62392:	gap of unknown length	*	137495	137494: gap of unknown length
65871:	gap of unknown length	*	137495	137494: gap of unknown length
65872:	contig of 2720 bp in length	*	137495	137494: gap of unknown length
68891:	gap of unknown length	*	137495	137494: gap of unknown length
68892:	contig of 1757 bp in length	*	137495	137494: gap of unknown length
70548:	gap of unknown length	*	137495	137494: gap of unknown length
70549:	contig of 2117 bp in length	*	137495	137494: gap of unknown length
72165:	gap of unknown length	*	137495	137494: gap of unknown length
72766:	contig of 3401 bp in length	*	137495	137494: gap of unknown length
76266:	gap of unknown length	*	137495	137494: gap of unknown length
76267:	contig of 2708 bp in length	*	137495	137494: gap of unknown length
76367:	gap of unknown length	*	137495	137494: gap of unknown length
79074:	contig of 2884 bp in length	*	137495	137494: gap of unknown length
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83557:	gap of unknown length	*	137495	137494: gap of unknown length
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87516:	contig of 2884 bp in length	*	137495	137494: gap of unknown length
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87616:	contig of 2797 bp in length	*	137495	137494: gap of unknown length
90413:	contig of 2797 bp in length	*	137495	137494: gap of unknown length
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93372:	contig of 3059 bp in length	*	137495	137494: gap of unknown length
93673:	gap of unknown length	*	137495	137494: gap of unknown length
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95740:	gap of unknown length	*	137495	137494: gap of unknown length
95841:	contig of 1452 bp in length	*	137495	137494: gap of unknown length
97293:	gap of unknown length	*	137495	137494: gap of unknown length
97393:	contig of 1108 bp in length	*	137495	137494: gap of unknown length
98800:	gap of unknown length	*	137495	137494: gap of unknown length
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10642:	contig of 1576 bp in length	*	137495	137494: gap of unknown length
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108043:	contig of 1726 bp in length	*	137495	137494: gap of unknown length
108044:	gap of unknown length	*	137495	137494: gap of unknown length
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111732:	contig of 1677 bp in length	*	137495	137494: gap of unknown length
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113205:	contig of 1892 bp in length	*	137495	137494: gap of unknown length
115196:	gap of unknown length	*	137495	137494: gap of unknown length
115297:	contig of 2076 bp in length	*	137495	137494: gap of unknown length
117373:	gap of unknown length	*	137495	137494: gap of unknown length
117472:	contig of 2576 bp in length	*	137495	137494: gap of unknown length
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122491:	contig of 2243 bp in length	*	137495	137494: gap of unknown length

Alignment Scores:  
 Pred. No.: 2.15e+03  
 Score: 44.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 DB: 2

US-09-698-781-17 (1-9) x AC094798 (1-153003)

AC020628 LOCUS AC020628 Homo sapiens chromosome 16 clone RP11-32B16, WORKING DRAFT DEFINITION Homo sapiens chromosome 16 clone RP11-32B16, WORKING DRAFT SEQUENCE, 7 unordered pieces.

ACCESSION AC020628 AC020628\_16 GI:14647255 VERSION AC020628\_16

KEYWORDS HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 161582)  
 AUTHORS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaralunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimark, K., Blantenburg, K., Bonin, D., Bouck, J., Bowie, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P., Buiay, C., Burch, P., Burkett, C., Burrill, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chodhray, I., Christopoulos, C.D., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.R., Delaney, K.M., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escott, M., Fails, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabiou, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Guaratine, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodson, A., Hogues, M., Holloway, C., Hollins, B., Homsli, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovari, C., Kratovic, J., Kurshia, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Licharge, O., Lieu, J., Liu, W., Louisel, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheeshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mathiney, E., McLeod, M.P., Meador, M., Mel, G., Metzker, M., Miner, G., Mitchell, T., Mobbabat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nickerson, E., Nwokenwo, S.,

		Alignment Scores:	2.27e+03	Length:	161582
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JOURNAL					
COMMENT	Worley K.C.				
AUTHORS	Worley, K.C., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.				
REFERENCE	Direct Submission				
JOURNAL	Unpublished				
COMMENT	2 (bases 1 to 161582)				
AUTHORS	Worley, K.C.				
REFERENCE	Direct Submission				
JOURNAL	Submitted (07-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA				
On Jul 10, 2001 this sequence version replaced gi:14600326.					
COMMENT					
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COMMENT	</td				

Consensus quality: 175928 bases at least Q20  
 Insert size: 180000; agarose-fp  
 Insert size: 17687; sum-of-contigs  
 Quality coverage: 10.5 in 020 bases; agarose-fp  
 Quality coverage: 10.7 in 020 bases; sum-of-contigs  
 ....  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 12 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 31880: contig of 31880 bp in length  
 \* 31881 31980: gap of 100 bp  
 \* 31981 32430: contig of 450 bp in length  
 \* 32431 32530: gap of 100 bp  
 \* 32531 33945: contig of 1415 bp in length  
 \* 33946 34045: gap of 100 bp  
 \* 34046 35388: contig of 1343 bp in length  
 \* -35389 35488: gap of 100 bp  
 \* 35489 41357: contig of 5869 bp in length  
 \* 41358 41477: gap of 100 bp  
 \* 41458 49412: contig of 7955 bp in length  
 \* 49413 49512: gap of 100 bp  
 \* 49513 58396: contig of 8884 bp in length  
 \* 58397 58496: gap of 100 bp  
 \* 58497 67955: contig of 9459 bp in length  
 \* 67956 68035: gap of 100 bp  
 \* 68056 115552: contig of 47497 bp in length  
 \* 115553 115552: gap of 100 bp  
 \* 115653 139731: contig of 24079 bp in length  
 \* 139732 139831: gap of 100 bp  
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 /db\_xref="taxon:10090"  
 /chromosome="6"  
 /map="6"  
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 /clone\_id="RPCI-23 Female Mouse BAC"  
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 misc\_feature  
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 /note="assembly\_fragment"  
 clone\_end:T7  
 BASE COUNT 48509 a 39454 c 38603 g 49318 t 1103 others  
 ORIGIN vector side:right  
 Alignment Scores:  
 Pred. No.: 2.49e+03  
 Score: 44.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 DB: 127402 ACCCTTTTCCGCTCTATCTCA 127376  
 RESULT 14  
 AC121977  
 LOCUS AC121977 229084 bp DNA linear HTG 21-MAY-2002  
 DEFINITION Mus musculus chromosome UNK clone RP24-28TA16, WORKING DRAFT  
 SEQUENCE, 8 unordered pieces.  
 ACCESSION AC121977  
 VERSION AC121977\_1 GI:21040100  
 KEYWORDS AC121977\_1 HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP;  
 SOURCE Mus musculus.  
 ORGANISM Mus musculus.  
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 TITLE The sequence of *Mus musculus* clone  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 229084)  
 AUTHORS McPherson,J.D. and Waterston,R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest Park  
 Parkway, St. Louis, MO 63108, USA  
 COMMENT -----  
 Center: Washington University Genome Sequencing Center  
 Center code: WIGSC  
 Web site: http://genome.wustl.edu/gsc/index.shtml  
 Contact: submissions@watson.wustl.edu  
 Center project name: M\_BB0287A16  
 -----  
 ----- Summary Statistics -----  
 Sequencing vector: M13; 0%  
 Sequencing vector: Plasmid; 100%  
 Chemistry: Dye-primer ET; 0% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 226270 bases at least Q40  
 Consensus quality: 226603 bases at least Q30  
 Consensus quality: 226772 bases at least Q20  
 Insert size: 222000; agarose-fp  
 Insert size: 228785; sum-of-contigs  
 Quality coverage: 14.73 in 020 bases; agarose-fp  
 Quality coverage: 10.44 in 020 bases; sum-of-contigs  
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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 8 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 5993: contig of 5993 bp in length  
 \* 1 6093: contig of 6927 bp in length  
 \* 6094 13020: contig of 6927 bp in length



15775 16611: contig of 867 bp in length  
 \* 16741 16761: gap of 100 bp  
 \* 17632 17731: gap of 100 bp  
 \* 17732 18666: contig of 915 bp in length  
 \* 18747 18747: gap of 100 bp  
 19638 19737: gap of 100 bp  
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 \* 20874 21133: contig of 860 bp in length  
 21734 21833: gap of 100 bp  
 \* 21834 22695: contig of 862 bp in length  
 22696 22795: gap of 100 bp  
 \* 23622 23722: contig of 827 bp in length  
 \* 23723 24055: contig of 883 bp in length  
 \* 24606 24705: gap of 100 bp  
 \* 24706 25554: contig of 869 bp in length  
 25575 25674: gap of 100 bp  
 \* 25675 26520: contig of 846 bp in length  
 \* 26521 26620: gap of 100 bp  
 \* 26621 27494: contig of 874 bp in length  
 \* 27495 27594: gap of 100 bp  
 \* 27595 28461: contig of 867 bp in length  
 28462 28561: gap of 100 bp  
 \* 29446 29545: gap of 100 bp  
 \* 29546 30421: contig of 876 bp in length  
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 \* 30522 31180: contig of 859 bp in length  
 31388 31480: gap of 100 bp  
 \* 32375 32475: contig of 894 bp in length  
 \* 32476 33445: gap of 100 bp  
 \* 33446 33480: contig of 835 bp in length  
 34281 34380: gap of 100 bp  
 \* 35231 35330: gap of 100 bp  
 \* 35331 36198: contig of 868 bp in length  
 36199 36298: gap of 100 bp  
 \* 36299 37169: contig of 871 bp in length  
 37170 37269: gap of 100 bp  
 \* 37270 38133: contig of 864 bp in length  
 38134 38233: gap of 100 bp  
 \* 38234 39116: contig of 893 bp in length  
 39117 39216: gap of 100 bp  
 \* 39217 40103: contig of 887 bp in length  
 40104 40203: gap of 100 bp  
 \* 40204 41074: contig of 871 bp in length  
 41075 41174: gap of 100 bp  
 \* 41175 42077: contig of 903 bp in length  
 \* 42078 42177: gap of 100 bp  
 \* 42178 43010: contig of 833 bp in length  
 43011 43110: gap of 100 bp  
 \* 43111 43394: contig of 884 bp in length  
 43995 44094: gap of 100 bp  
 \* 44095 44165: contig of 871 bp in length  
 \* 44966 45065: gap of 100 bp  
 \* 45066 45539: contig of 874 bp in length  
 45940 46039: gap of 100 bp  
 \* 46040 46528: contig of 899 bp in length  
 46929 47028: gap of 100 bp  
 \* 47029 47781: contig of 883 bp in length  
 \* 47882 47981: gap of 100 bp  
 \* 47982 48855: contig of 874 bp in length  
 48856 48955: gap of 100 bp  
 \* 48956 49550: contig of 895 bp in length  
 49851 49950: gap of 100 bp  
 \* 49951 50825: contig of 875 bp in length  
 50826 50925: gap of 100 bp  
 \* 50926 51181: contig of 836 bp in length

FEATURES  
Source

BASE COUNT 15372 a 10594 c 10818 g 15552 t 6222 others  
ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Length:	Score:	Length:	Matches:	Length:	Score:	Length:	Matches:
	Percent Similarity:	43.00	43.00	Percent Similarity:	0.00%	Percent Similarity:	0.00%	Percent Similarity:	0.00%	Percent Similarity:	0.00%
	Best Local Similarity:	88.89%	88.89%	Best Local Similarity:	88.89%	Best Local Similarity:	88.89%	Best Local Similarity:	88.89%	Best Local Similarity:	88.89%
Query Match:	97.73%			Query Match:		Query Match:		Query Match:		Query Match:	
DB:		2		DB:		DB:		DB:		DB:	
	Gaps:	0			Gaps:	0			Gaps:	0	

US-09-698-781-17 (1-9) x AC024305 (1-55558)  
 QY 1 ThrIeupPhaProValLeuLeuPhaLeu 9  
 |||||:|||||:|||||:|||||:|||||:  
 Db 30338 ACCCTTTCCATATTATTCCTT 30312

Search completed: March 14, 2003, 04:41:17  
 Job time : 213.888 secs